



VHL/E	1	ATGACACCGACGACGACGACCGCGGAACTCACG	33
VHL/E	34	ACGGAGTTTGACTACGACGATGAAGCGACTCCC	66
VHL/E	67	TGTGTCCTCACCGACGTGCTTAATCAGTCGAAG	99
VHL/E	100	CCAGTCACGTTGTTTCTGTACGGCGTTGTCTTT	132
VHL/E	133	CTCTTCGGTTCCATCGGCAACTTCTTGGTGATC	165
VHL/E	166	TTCACCATCACCTGGCGACGTCGGATTCAATGT	198
VHL/E	199	TCCGGCGATGTTTACTTTATCAACCTCGCGGCC	231
VHL/E	232	GCCGATTTGCTTTTCGTTTGTACACTACCTCTG	264
VHL/E	265	TGGATGCAATACCTCCTAGATCACAACCTCCCTA	297
VHL/E	298	GCCAGCGTGCCGTGTACGTTACTCACTGCCTGT	330
VHL/E	331	TTCTACGTGGCTATGTTTGCCAGTTTGTGTTTT	363
VHL/E	364	ATCACGGAGATTGCACTCGATCGCTACTACGCT	396
VHL/E	397	ATTGTTTACATGAGATATCGGCCTGTAAAACAG	429
VHL/E	430	GCCTGCCTTTTCAGTATTTTTTTGGTGGATCTTT	462
VHL/E	463	GCCGTGATCATCGCCATTCCACACTTTATGGTG	495
VHL/E	496	GTGACCAAAAAAGACAATCAATGTATGACCGAC	528
VHL/E	529	TACGACTACTTAGAGGTCAGTTACCCGATCATC	561
VHL/E	562	CTCAACGTAGAACTCATGCTCGGTGCTTTCGTG	594
VHL/E	595	ATCCCGCTCAGTGTCATCAGCTACTGCTACTAC	627
VHL/E	628	CGCATTTCCAGAATCGTTGCGGTGTCTCAGTCG	660
VHL/E	661	CGCCACAAAGGCCGCATTGTACGGGTACTTATA	693
VHL/E	694	GCGGTGCTGCTTGTCTTTATCATCTTTTGGCTG	726
VHL/E	727	CCGTACCACCTGACGCTGTTTGTGGACACGTTG	759
VHL/E	760	AAACTGCTCAAATGGATCTCCAGCAGCTGCGAG	792
VHL/E	793	TTCGAAAAATCACTCAAGCGCGCGCTCATCTTG	825
VHL/E	826	ACCGAGTCACTCGCCTTTTGTCACTGTTGTCTC	858
VHL/E	859	AATCCGCTGCTGTACGTCTTCGTGGGCACCAAG	891
VHL/E	892	TTTCGGCAAGAACTGCACTGTCTGCTGGCCGAG	924
VHL/E	925	TTTCGCCAGCGACTGTTTTCCCGCGATGTATCC	957
VHL/E	958	TGGTACCACAGCATGAGCTTTTCGCGTCGGAGC	990
VHL/E	991	TCGCCGAGCCGAAGAGAGACGTCTTCCGACACG	1023
VHL/E	1024	CTGTCCGACGAGGCGTGTCGCGTCTCACAAATT	1056
VHL/E	1057	ATACCGTAA	1065

FIG. 1A



VHL/E	1	<u>MTPTTTTAELTTEFDYDDEATPCVLT</u> <u>DVLNQSK</u>	33
VHL/E	34	<u>PVTLFLYGVVFLFGSIGNFLVIFTITWRRRIQC</u>	66
VHL/E	67	SGDVYFINLAAADLLFVCTLPLWMQYLLDHNSL	99
VHL/E	100	ASVPCTLLTACFYVAMFASLCFITEIALDRYYA	132
VHL/E	133	IVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMV	165
VHL/E	166	VTKKDNQCMTDYDYLEVSYPIILNVELMLGAFV	198
VHL/E	199	IPLSVISYCYRISRIVAVSQSRHKGRIVRVLI	231
VHL/E	232	AVVLVFIIFWLPYHLTLFVDTLKLLKWISSSCE	264
VHL/E	265	FEKSLKRALILTESLAFCHCCLNPLLYVFGTK	297
VHL/E	298	FRQELHCLLAEFRQRLFSRDVSWYHSMFSRRS	330
VHL/E	331	SPSRRETSSDTLSDEACRVSQIIP	354

FIG. 1B



Replacement Sheet

human US28	1	MTPTT	- - - - -	5
rhesus US28.1	1	M	- - - - -	1
rhesus US28.2	1	MTNA	- - - - -	4
rhesus US28.3	1	MTNT	- - - - -	4
rhesus US28.4	1	M	- - - - -	0
rhesus US28.5	1	MTTTTMSATTNSSTTPQASSTTMTTKTSTPGN		32
human US28	6	- - - TTAELTT	- - - - -	12
rhesus US28.1	2	- - - - -	- - - - -	1
rhesus US28.2	5	- - - - -	- - - - -	4
rhesus US28.3	5	- - - - -	- - - - -	4
rhesus US28.4	1	- - - - -	- - - - -	0
rhesus US28.5	83	TTTGTTSTLTTISTTSNATSITSNLSTTGNQT		64
human US28	13	- - - - -	- - - - -	12
rhesus US28.1	2	- - - - -	- - - - - NNT	4
rhesus US28.2	5	- - - - -	- - - - - GH-	6
rhesus US28.3	5	- - - - -	- - - - - NNT	7
rhesus US28.4	1	- - - - -	- - - - - NSSQHNISVFLSIGA-	15
rhesus US28.5	65	ATTNATTFSSSTLTTSTNISSTFSTVSTVASNA		96
human US28	13	- - - - -	- - - - -	12
rhesus US28.1	5	SCN	- - - - - F	8
rhesus US28.2	7	CH	- - - - - I	9
rhesus US28.3	8	TCH	- - - - - L	11
rhesus US28.4	16	- - - - -	- - - - - GPVITG-	21
rhesus US28.5	97	TCNSTITTNITTAFTTAANTTASSLTSIVTSL		128
human US28	13	- - - - - EFDYDEDATPCVFETDVLNQSKPVTLL		37
rhesus US28.1	9	NVTLNASSA	- - - - - PSRYIAI	23
rhesus US28.2	10	NE SLASYG	- - - - - IAPAATI	24
rhesus US28.3	12	NGTFETF[K]	- - - - - ITRPVAI	26
rhesus US28.4	22	- - - - -	- - - - -	21
rhesus US28.5	129	ATTIETTSEFDYDESAEACNLTDIVHTTRSVTV		160

FIG. 2A

human US28	38	F L Y G V V F L F G S I G N F - L V I F T I T W R R R I O C S G	68
rhesus US28.1	24	A M Y S I V I C I G L V G N L L L C I V L V K - K R K L R Y S S	54
rhesus US28.2	25	T L Y S I A G I C G V T G N L L I L L V L F T - R R I H W F A N	55
rhesus US28.3	27	S A Y T V L V V I G L L G N I V L L S V L V V - K R K L K F P N	57
rhesus US28.4	22	- - Y T C V F L F G I L G H F Y L Y W K N H Q R R H R T N S F S	51
rhesus US28.5	61	T F Y T I I F I L G L L G N F - L V L M T I I W N R R I S F M V	191
human US28	69	D V Y F I N L A A A D L L F V C T L P L W M Q Y L L D H N S L A	100
rhesus US28.1	55	D V Y F F H A S M A D L V S T V M L P L W L H Y V L N F A Q L S	86
rhesus US28.2	56	D I Y Y L N M I F T D F L V F I T L P A W V Y Y L L N Y T Q L S	87
rhesus US28.3	58	D I Y F F N A S L A D V F A V C M L P A W V N Y A L D S T Q L S	89
rhesus US28.4	52	D V L F R H L M I T E E V F T L T I P V W A Y H L T T H G N L P	83
rhesus US28.5	192	E I Y F V N L A I S D L M F V C T L P F W I M Y L L E H D V M S	223
human US28	101	S V P C T L L T A C F Y V A M F A S L C F I T E I A L D R Y Y A	132
rhesus US28.1	87	R G A C I S F S V T F Y V P L F V Q A W L L I S I A M E R - Y S	117
rhesus US28.2	88	H Y A C I A L S F V F Y V S I F I Q A D F M V A V A I E R - Y R	118
rhesus US28.3	90	K F S C I T F T F G F Y V S L F I Q A W M L I L V T L E R - Y G	120
rhesus US28.4	84	G S W C R S L T F V F Y L T V F A R A F F Y L L L I W D R - Y S	114
rhesus US28.5	24	H A S C V A M T A I F Y C A L F A S T V F L L L I V L D R C Y A	255
human US28	133	I V Y M R Y R P V K Q - - - - - A C L F S I F W W I F A V I	157
rhesus US28.1	118	N L V W M A P I S V K - - - T A F K H C I G T - - - W I V S A F	143
rhesus US28.2	119	S L V K N K P L S V K - - - K A S V S C A C I - - - W I I V I I	144
rhesus US28.3	121	S L V W I A P I T R N - - - K A I A N C V L F - - - W L V S I F	146
rhesus US28.4	115	V I I C R H P L P V N L N Y S Q V I G - - - L S V W - - L V A V	141
rhesus US28.5	256	I L L G T E K A N R R L L R N A V S G C M L M - - - W G L C F I	284
human US28	158	I A I P H F M V V T K - K D N Q C - M T D Y D Y - L E V S Y P I	186
rhesus US28.1	144	V A S P Y Y A Y R N S H D E H E C I L G N Y T W H I N E P L H T	175
rhesus US28.2	145	V S S P Y Y M F R S Q H E T N S C I L G N Y T W H M N S P F R T	176
rhesus US28.3	147	L A A P Y Y S F R N E S N E H Q C I M R N Y T W S V G E T W H I	178
rhesus US28.4	142	L S A S P F S I F N G - S V K Q C - L G N M G - S I P S E S S A	170
rhesus US28.5	285	L A L P H F I F M K K - G T N V C - V A E Y E P G L N N F Y V I	314

FIG. 2B



human US28	187	I L N V E L M L G A F V I P L S V I S Y C Y Y R I S R I V A V S	218
rhesus US28.1	176	C M D M V I I V W T F L A P V L V T I I A S V K M - R R T T W G	206
rhesus US28.2	177	T M D A S I N I W S F V V P A V T T L I A R R I Y V - C T S G	207
rhesus US28.3	179	A L D F L I T L I T F I M P V T I V L A L S F K M A R W S T F G	210
rhesus US28.4	171	V L N L E V H L C S F W L P L I M S A N C Y Y Q A K R R A S P D	202
rhesus US28.5	245	F I N T E V N L C T L V L P A A A I I Y W Y L K L T K A L K T H	346
human US28	219	Q S - R H K G R I V R V L I A V V L V F I I F W L P Y H L T L F	249
rhesus US28.1	207	N T - R L N E K N S D I L I V L V V M T V F F W G P F N I V L V	237
rhesus US28.2	208	N K - K M N A R A S G L L E A M V I S M L F F G G L F N L N I F	238
rhesus US28.3	211	Y R - N L T S R T S L I L I L I L T V A A G F W G P F H L F M F	241
rhesus US28.4	203	Q - - L H E L Y R C S L L I T I I T T Y A I V W F P F H L A L L	232
rhesus US28.5	347	E R L R H R L T S L N I V L A V V I V F A L F W L P Y N L M L M	378
human US28	250	V D T L K L - L K W I S S S C E F E R S L K R A L I L T E S L A	280
rhesus US28.1	238	I D N I L Q R Y Y D T - T N C D V E K I K H I M A M I S E A I V	268
rhesus US28.2	239	R D - I V S D T S E D N K D C T Y L K Q E H F I R M V G V A L V	269
rhesus US28.3	242	I E N M A G Q I Y H I Q K D C W Y L Q L R H L C S L M T E T L V	273
rhesus US28.4	233	I D A L I S - I S H V E P S S A L H W A - - S I V V T C K S F T	261
rhesus US28.5	379	M Y S L V H - M Q - I P W E C S S E K I L R R S L I I T E S I A	408
human US28	281	F C H C C L N P L L Y V F V G T K F R Q E L H C L L A E F R Q R	312
rhesus US28.1	269	Y F R G I T A P I I Y V G I S G R F R E E I Y S L F R R Q P Y N	300
rhesus US28.2	270	Y G R A I F N P F M Y M C V S T R L R Q E I K C L F M R I P Y E	301
rhesus US28.3	274	F L R S V F N P Y I Y M I I S Y K F R Q Q V R S L L K R T Q Y D	305
rhesus US28.4	262	F V Y A G I S P L V Y F T C C P T V R R E L L M S L R P F F T -	292
rhesus US28.5	409	L S H C C I N P I I Y L L F G P R C R S E F C H L L R C C F T R	440
human US28	313	L F S R D V S W - - Y H S M S F S R R S S P S R R E T S S D T L	342
rhesus US28.1	301	D L D P D A N - - - - Q F M I E L T S Q G R S R N R N A R Q S	327
rhesus US28.2	302	T L D A E H A - - - - K L M V N L K N R N A N V P D P K - - -	325
rhesus US28.3	306	A L D T T Q L - - - - A E T M Q L K A K G V P V S D P A - - -	329
rhesus US28.4	293	- - - - - W I S S K T R R G Y A P I K T Q P L N I P D E P I	317
rhesus US28.5	441	L - C P H R S W S S I R A E T V S I S L S H S Q V S A S S E D D	471
human US28	343	S D E V C R V S Q I I P	354
rhesus US28.1	328	E S N V P Q P E E C F W	339
rhesus US28.2	326	- - - - P R E Y E S V L	333
rhesus US28.3	380	- - - - P H D C E C F L	337
rhesus US28.4	318	D N K S P H L L N - - E	327
rhesus US28.5	472	D N D V H D E L Q F L I	483

FIG. 2C



## Replacement Sheet

human UL78	1	MSPSVEETTSVTESIMFAIVSFKHMGPFEgy	31
rhesus UL78	1	- - - - -	0
human UL78	32	SMSADRAASDLLIGMFSGVSLVNLTLTIGCL	62
rhesus UL78	1	-MITERVLAGILAGMTAAGSLVILLAVV--M	28
human UL78	63	WVLRVTRP--PVSVMIFTWNLVLSQFFSILA	91
rhesus UL78	29	WLNMLDRAGMMAVGHYTGNLVLTQVICIFS	59
human UL78	92	TMLSKGIMLRGALNLSLCRLVLFVDDVGLYS	122
rhesus UL78	60	-MLASKIVGMTSAANMGFCGIVVFLEDTGLY	89
human UL78	123	TALFFLFLILDRLSAISYGRDLWHHE-TREN	152
rhesus UL78	90	VTSLLFMFMI LDRMAAFLNGRLFWRQQTTKQ	120
human UL78	153	AGVALYAVAFAWVLSIVAAPTAATGSLDYR	183
rhesus UL78	121	NLSTSVYIILFCWVLGMAAAVPSAAVAAPNS	151
human UL78	184	WLGCIPIQYAAVDLTIKMWFLLGAPMIAVL	214
rhesus UL78	152	RWERCEIPVSYAAIDMIVKLWVLLAPVVL I	182
human UL78	215	ANVVELAYSDDRHDVWSYVGRVCTFYVTCLM	245
rhesus UL78	183	MAV I IQSSYHRDRERI WYARRVFMFYTACF	213
human UL78	246	LFVPYYCFRV-----LRGV-LQPASAA GTG	269
rhesus UL78	214	VMMVPYYFVRVMLSDFALVDIKTKTANS DGC	244
human UL78	270	FGIMDYVELATRTLTLTMR LGILPLFI I A FFS	300
rhesus UL78	245	DSTFLDYLNMFTHVIYSFKLVVFALFIVLFC	275
human UL78	301	REPTKDLDDSF DYLVERCQQSCHGHFVRRLV	331
rhesus UL78	276	SINPMETLEECLERADAERQSRSEASQGERR	306
human UL78	332	QALKRAMYSVELAVCYFSTSVRDVAEAVKKS	362
rhesus UL78	307	LPINTCCI KLIELIKQYVSTLSKATRDN SGE	337
human UL78	363	SSRCYADATSAAVVVT TTTSEKATLVEHAEG	393
rhesus UL78	338	RANLPENAEDIGTTGSDQLPTEVTVT PNSSA	368
human UL78	394	MASEMCPGTTIDVSAESSSVLCTDGEN TVAS	424
rhesus UL78	369	VFSTGGTVSPV	379
human UL78	425	DATVTAL	431

FIG. 3



Replacement Sheet

H UL33	1	M	- - - - -	1
HUL33splice	1	MDTIIHNSI	- - - - -	9
RhUL33	1	M	- - - - -	1
RhUL33splice	1	MAVTLRGGSPINFKLMIVSHRNRKFHEIRLFQ		32
H UL33	2	- - - - -	- - - - -	1
HUL33splice	10	RNNTPP	- - - - - HINDTCNM	23
RhUL33	2	- - - - -	- - - - -	1
RhUL33splice	33	RSAIRPGGLWKPFFTTERETNSILHINTTCNV		64
H UL33	2	TGPLFAIRTTTEAVLNTFIIIFVGGPLNAIVLIT		33
HUL33splice	24	TGPLFAIRTTTEAVLNTFIIIFVGGPLNAIVLIT		55
RhUL33	2	- - - - -	- - - - -	1
RhUL33splice	65	TDSL YAAKLG EALVNSALALFGTPLNAIVLVT		96
H UL33	34	QLLTNRVLGYSTPTIYMTNLYSTNFLTTLTVLP		65
HUL33splice	56	QLLTNRVLGYSTPTIYMTNLYSTNFLTTLTVLP		87
RhUL33	2	- - - - - TNLYSANFLTTLIVLP		16
RhUL33splice	97	QLLANRVHGYSTPIIYMTNLYSANFLTTLIVLP		128
H UL33	66	PIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF		97
HUL33splice	88	PIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF		119
RhUL33	17	PIVLSNQHLLPASAVTCKFLSLLYYSSCSVGF		48
RhUL33splice	129	PIVLSNQHLLPASAVTCKFLSLLYYSSCSVGF		160
H UL33	98	ATVALIAADRYRVLHKRTYARQSYRSTYMI LL		129
HUL33splice	120	ATVALIAADRYRVLHKRTYARQSYRSTYMI LL		151
RhUL33	49	ATVALIAADRYRVIHRRRTQARQSYRN TYMIVG		80
RhUL33splice	161	ATVALIAADRYRVIHRRRTQARQSYRN TYMIVG		192
H UL33	130	LTWLAGLIFSVPAAVYTTVVMHHDANDTNNTN		161
HUL33splice	152	LTWLAGLIFSVPAAVYTTVVMHHDANDTNNTN		183
RhUL33	81	LTWLI GLI CATPGGVYTTI VAHRDGE - - SDAQ		110
RhUL33splice	193	LTWLI GLI CATPGGVYTTI VAHRDGE - - SDAQ		222

FIG. 4A



Replacement Sheet

H UL33	162	GHATCVLYFVAEEVHTVLLSWKVLLTMWVGAA	193
HUL33splice	184	GHATCVLYFVAEEVHTVLLSWKVLLTMWVGAA	215
RhUL33	111	RHNNTCIMHFAYDEVY-VLMVWKLLIVLVWGI V	141
RhUL33splice	223	RHNNTCIMHFAYDEVY-VLMVWKLLIVLVWGI V	253
H UL33	194	PVIMMTWIFYAFFYSTVQRTSLKQRSRTLTFVS	225
HUL33splice	216	PVIMMTWIFYAFFYSTVQRTSLKQRSRTLTFVS	247
RhUL33	142	PVVMMSWIFYAFFYNTVQRTAKKKQQ-RTLKFVK	172
RhUL33splice	254	PVVMMSWIFYAFFYNTVQRTAKKKQQ-RTLKFVK	284
H UL33	226	VLLISFVALQTPYVSLMIFNSYATTAWPMQCE	257
HUL33splice	248	VLLISFVALQTPYVSLMIFNSYATTAWPMQCE	279
RhUL33	173	VLLLSFII IQTPYVSIMIFNTYATVGWPM ECA	204
RhUL33splice	285	VLLLSFII IQTPYVSIMIFNTYATVGWPM ECA	316
H UL33	258	HLTLRRTIGTLARVVPHLHCLINPILYALLGH	289
HUL33splice	280	HLTLRRTIGTLARVVPHLHCLINPILYALLGH	311
RhUL33	205	DLTRRRRVINTFSRLVPNLHCMVNPILYALMGN	236
RhUL33splice	317	DLTRRRRVINTFSRLVPNLHCMVNPILYALMGN	348
H UL33	290	DFLQRMQRQCFRGQLLDRAFLRSQNNQRATAE	321
HUL33splice	312	DFLQRMQRQCFRGQLLDRAFLRSQNNQRATAE	343
RhUL33	237	DFVSKVGQCFRGELTNRRRTFLRSKQQARNSSDD	258
RhUL33splice	349	DFVSKVGQCFRGELTNRRRTFLRSKQQARNSSDD	380
H UL33	322	TNLAAGNNSQSVATSLDTNSKNYNQHAKRSVS	353
HUL33splice	344	TNLAAGNNSQSVATSLDTNSKNYNQHAKRSVS	375
RhUL33	269	VPTIVSQQP-ATPTIVNKPEK--NPHVKRGVS	297
RhUL33splice	381	VPTIVSQQP-ATPTIVNKPEK--NPHVKRGVS	409
H UL33	354	FNFPSTGWKGGQKTASNDTSTKIPHRLSQSHH	385
HUL33splice	376	FNFPSTGWKGGQKTASNDTSTKIPHRLSQSHH	407
RhUL33	298	FSVSASSELA AAKKAKDKA- - - -KRLSM SHQ	324
RhUL33splice	410	FSVSASSELA AAKKAKDKA- - - -KRLSM SHQ	436
H UL33	386	NLSGV	390
HUL33splice	408	NLSGV	412
RhUL33	325	NLR LT	329
RhUL33splice	437	NLR LT	441

FIG. 4B



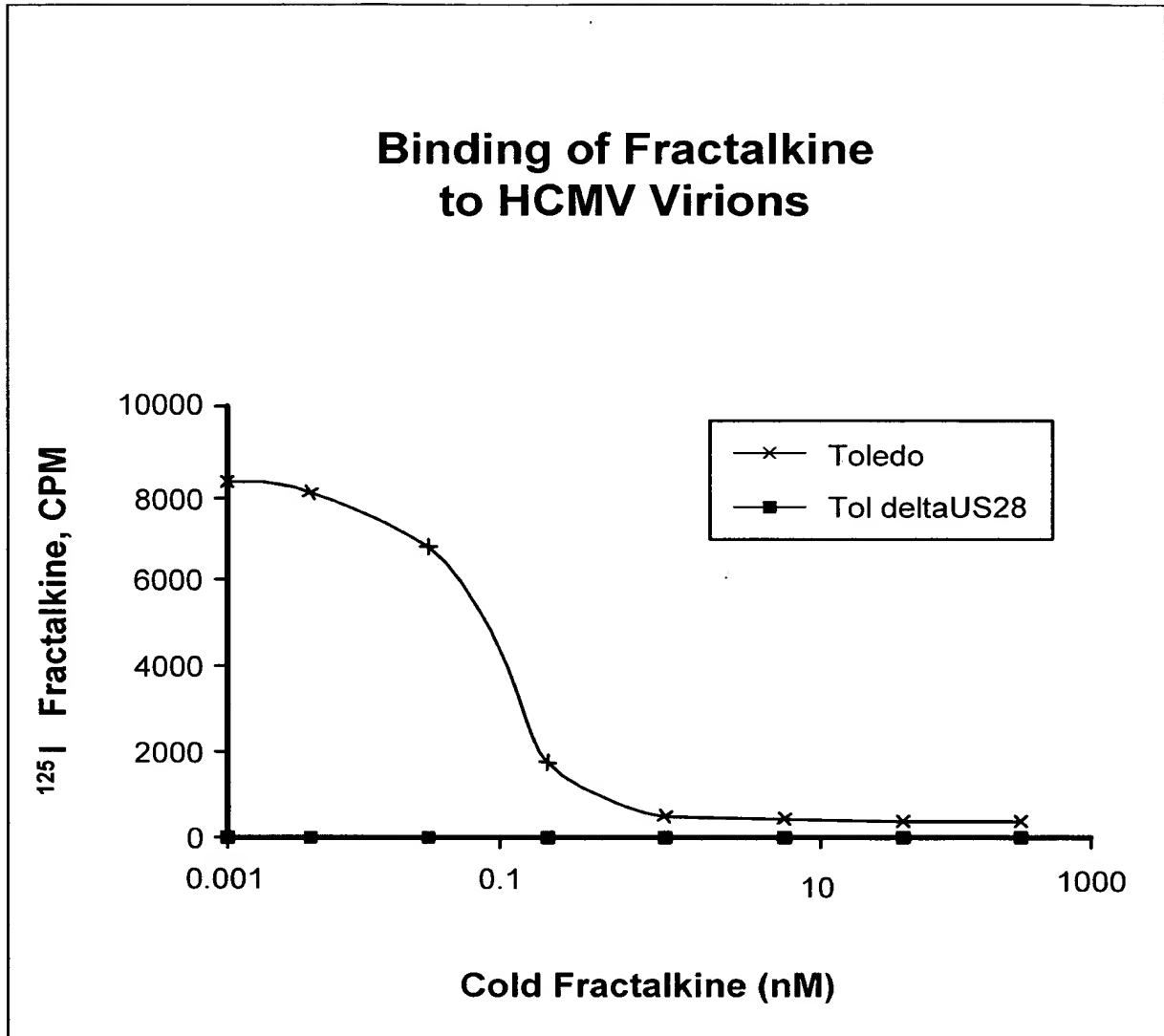


FIG. 5



### Fractalkine Homologous Competition on Rh-CMV Infected Fibroblasts

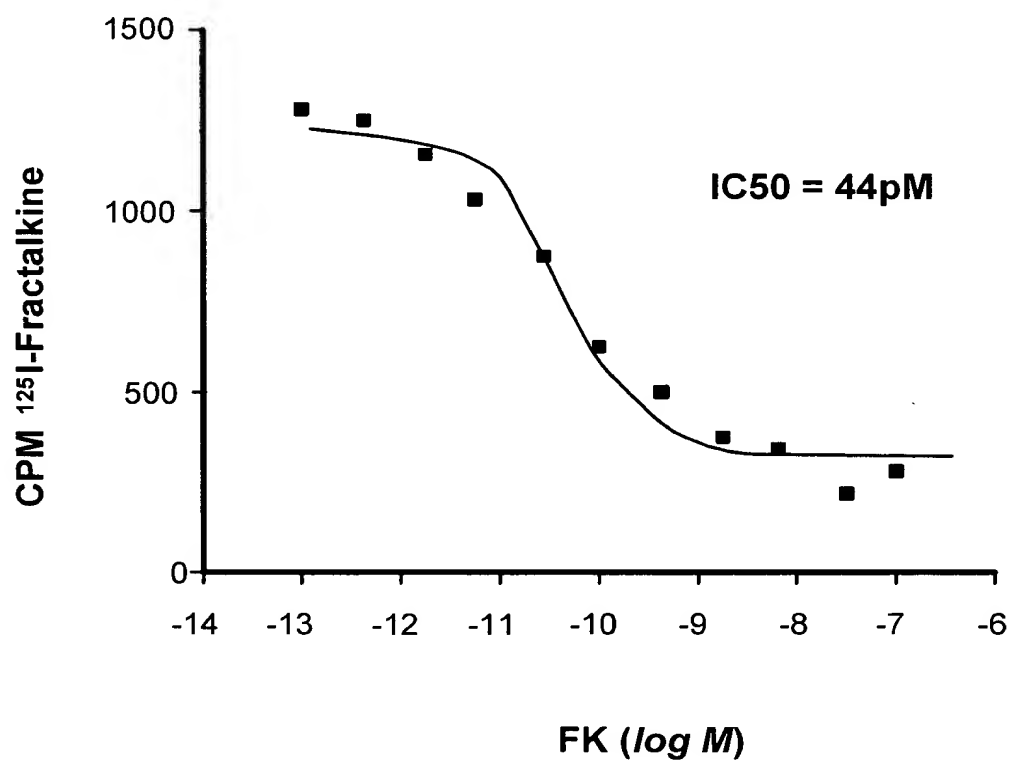


FIG. 6

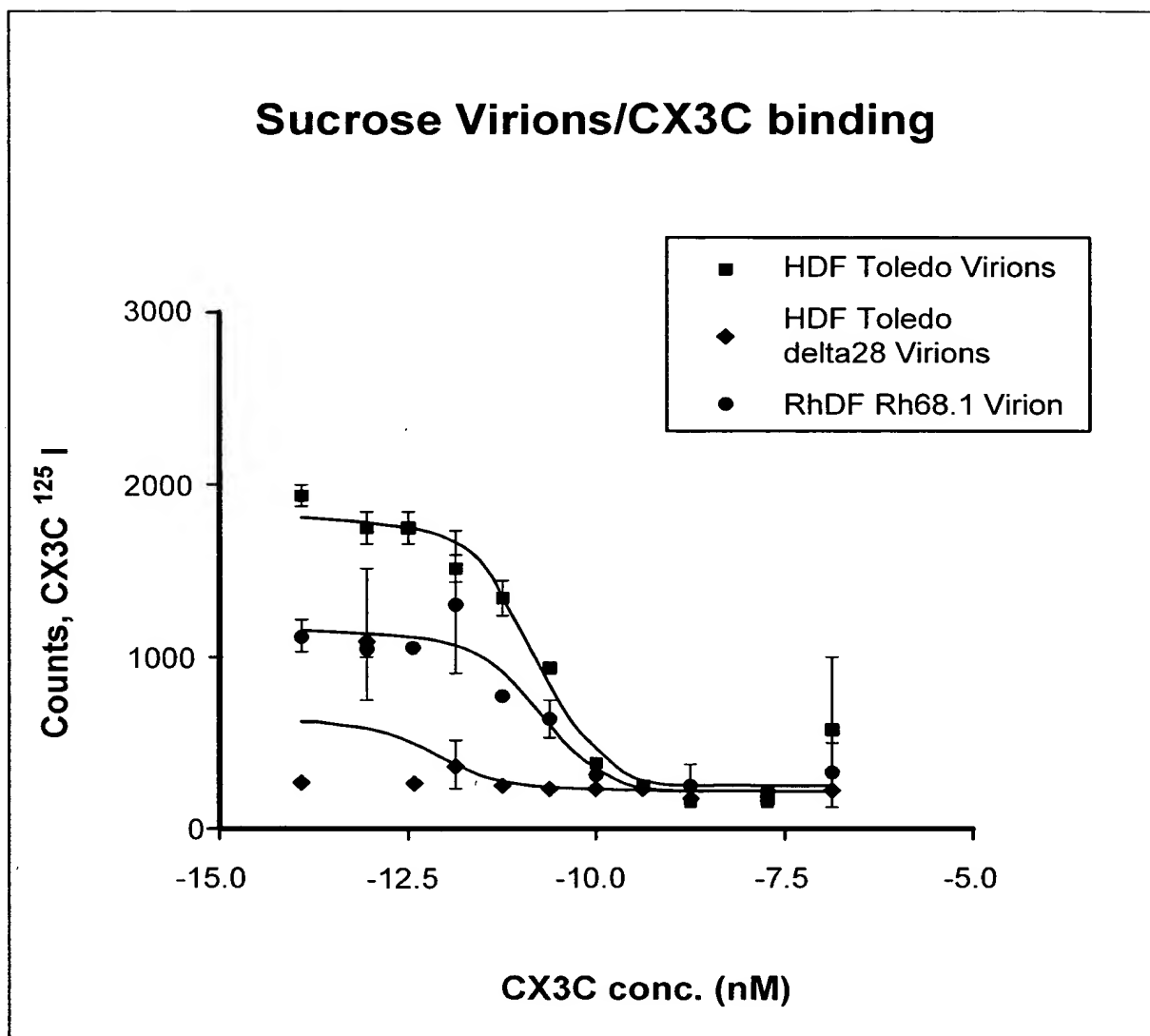


FIG. 7